

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:39 ; Search time 2351.15 Seconds  
(without alignments)  
154.366 Million cell updates/sec

Title: US-09-851-670-13

Perfect score: 22  
Sequence: 1 caccgcctctcgcacatgga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 segs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_om: \*  
20: em\_or: \*  
21: em\_ov: \*  
22: em\_pat: \*  
23: em\_ph: \*  
24: em\_pl: \*  
25: em\_ro: \*  
26: em\_sts: \*  
27: em\_sy: \*  
28: em\_un: \*  
29: em\_vi: \*  
30: em\_htgo\_hum: \*  
31: em\_htgo\_inv: \*  
32: em\_htg\_rod: \*  
33: em\_htg\_hum: \*  
34: em\_htg\_inv: \*  
35: em\_htg\_rod: \*  
36: em\_htg\_other: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	13.4	60.9	41	6	A93667	A93667 Sequence 3
2	13	59.1	37	6	A98891	A98891 Sequence 9
3	12.8	58.2	35	6	AR059842	AR059842 Sequence
4	12.8	58.2	57	9	S57433	S57433 T-cell-rece
5	12.6	57.3	37	6	A98888	A98888 Sequence 6
6	12.6	57.3	48	3	HC084486	HC084486 Haemochus
7	12.6	57.3	58	6	118948	118948 Sequence 30
8	12.6	57.3	58	6	118949	118949 Sequence 31
9	12.6	57.3	58	6	124133	124133 Sequence 30
10	12.6	57.3	58	6	124134	124134 Sequence 31
11	12.4	56.4	40	6	AR150948	AR150948 Sequence
12	12.4	56.4	42	6	AR123052	AR123052 Sequence
13	12.4	56.4	51	6	AR118585	AR118585 Sequence
14	12.2	55.5	27	6	AR153624	AR153624 Sequence
15	12.2	55.5	51	6	A42067	A42067 Sequence 10
16	12.2	55.5	51	6	AX160849	AX160849 Sequence
17	12.2	55.5	60	6	AR0463	AR0463 Sequence 23
18	12	54.5	31	6	140626	140626 Sequence 3
19	12	54.5	49	6	108645	108645 Sequence 1
20	12	54.5	51	9	S78430	S78430 Homo sapien
21	12	54.5	57	9	HSTCK6X13	HSTCK6X13 Sequence
22	12	54.5	57	9	HSTCK6X35	HSTCK6X35 Sequence
23	12	54.5	57	9	HSTCK6X36	HSTCK6X36 Sequence
24	12	54.5	57	9	HSTCK6X13	HSTCK6X13 Sequence
25	12	54.5	57	9	HSTCK6X35	HSTCK6X35 Sequence
26	12	54.5	57	9	HSTCK6X36	HSTCK6X36 Sequence
27	11.8	53.6	26	6	179834	179834 Sequence 19
28	11.8	53.6	32	6	AR054995	AR054995 Sequence
29	11.8	53.6	32	6	AR156244	AR156244 Sequence
30	11.8	53.6	36	6	186428	186428 Sequence 36
31	11.6	52.7	20	6	AR129487	AR129487 Sequence
32	11.6	52.7	20	6	E31432	E31432 Gene partic
33	11.6	52.7	27	6	AR008922	AR008922 Sequence
34	11.6	52.7	27	6	AR087617	AR087617 Sequence
35	11.6	52.7	28	6	182037	182037 Sequence 75
36	11.6	52.7	28	6	191725	191725 Sequence 75
37	11.6	52.7	35	6	A17073	A17073 Oligonucleo
38	11.6	52.7	35	6	A17074	A17074 Oligonucleo
39	11.6	52.7	35	6	A17471	A17471 Oligonucleo
40	11.6	52.7	35	6	A17472	A17472 Oligonucleo
41	11.6	52.7	35	6	A23883	A23883 Oligonucleo
42	11.6	52.7	35	6	A23899	A23899 Oligonucleo
43	11.6	52.7	35	6	AR014441	AR014441 Sequence
44	11.6	52.7	35	6	AR014450	AR014450 Sequence
45	11.6	52.7	35	6	AR059828	AR059828 Sequence

## ALIGNMENTS

RESULT	1	LOCUS	A93667	41 bp	DNA	PAT	22-JAN-2000
DEFINITION	Sequence 3 from Patent WO9734144.						
ACCESSION	A93667						
VERSION	A93667.1	GI:6741855					
KEYWORDS							
SOURCE							
ORGANISM	synthetic construct.						
REFERENCE	artificial sequence.						
AUTHORS	1 (bases 1 to 41)						
TITLE	LANGER, G. and TOSCHL, L.						
JOURNAL	PATENT: WO 9734144-A 3 18-SEP-1997;						
FEATURES	SCHERING AG (DE); LANGER GERNOT (DE)						
SOURCE	Location/Qualifiers						
	1..41						
	/organism="synthetic construct"						
	/db_xref="taxon:32630"						

BASE COUNT 5 a 14 c 15 g 7 t  
ORIGIN

Query Match 60.9%; Score 13.4; DB 6; Length 41;  
Best Local Similarity 93.3%; Pred. No. 1.6e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 caccgcgtctctcga 15  
|||||  
Db 31 CACCCGCTTCTCGA 17

RESULT 2  
LOCUS A98891 37 bp DNA PAT 26-JAN-2000  
DEFINITION Sequence 9 from Patent WO909211.  
ACCESSION A98891  
VERSION A98891.1 GI:6781850  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 37)  
AUTHORS Coutts,J.C. and Oultram,J.D.  
TITLE AMPLIFICATION OF NUCLEIC ACIDS  
JOURNAL Patent: WO 909211-A 9 25-FEB-1999;  
COUTTS JACQUELINE CLARE (GB); OULTRAM JOHN DOUGLAS (GB)  
FEATURES  
source 1..37  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 9 a 8 c 9 g 11 t  
ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 37;  
Best Local Similarity 76.2%; Pred. No. 2.7e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 accgcgtctctcgacaatga 22  
|||||  
Db 8 AACCACTGCTCGACGCTGA 28

RESULT 3  
LOCUS AR059842 35 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 50 from patent US 5840521.  
ACCESSION AR059842  
VERSION AR059842.1 GI:5986292  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Barth,P.Thomas.  
TITLE Expression vector containing an inducible selection gene system  
JOURNAL Patent: US 5840521-A 50 24-NOV-1998;  
FEATURES  
source 1..35  
/organism="unknown"  
BASE COUNT 10 a 7 c 9 g 9 t  
ORIGIN

Query Match 58.2%; Score 12.8; DB 6; Length 35;  
Best Local Similarity 87.5%; Pred. No. 3.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 gctctcgcacaatgg 21  
|||||  
Db 22 GCTCTCTAGACCATGG 7

RESULT 4  
LOCUS S57433 57 bp mRNA PRI 07-MAY-1993  
DEFINITION T-cell-receptor Valpha 17.2 segment [human, mRNA Partial, 57 nt].  
ACCESSION S57433  
VERSION S57433.1 GI:236318  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 57)  
AUTHORS Nematsu,Y., Wege,H., Straus,A., Ott,M., Bannwarch,W., Lanchbury,J.,  
Panayi,G. and Steinmetz,M.  
TITLE The T-cell-receptor repertoire in the synovial fluid of a patient  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (19), 8534-8538 (1991)  
MEDLINE 9202087  
REMARK Genbank staff at the National Library of Medicine created this  
entry [NCBI glibsg 57433] from the original journal article.  
This sequence comes from Fig 3.  
FEATURES  
source 1..57  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
1..57  
/partial  
/gene="T-cell-receptor Valpha 17.2 segment"  
1..57  
/partial  
/gene="T-cell-receptor Valpha 17.2 segment"  
/note="This sequence comes from Fig 3"

CDS  
/product="T-cell-receptor variable region alpha chain C terminus"  
/protein\_id="AAB19956.1"  
/db\_xref="GI:236319"  
/translation="LSLDIVPSQPDSDANYFCA"

BASE COUNT 8 a 20 c 12 g 17 t  
ORIGIN

Query Match 58.2%; Score 12.8; DB 9; Length 57;  
Best Local Similarity 87.5%; Pred. No. 3.5e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 cgctctcgcacaatg 20  
|||||  
Db 1 CTCTCTCTCGACATGG 16

RESULT 5  
LOCUS A98888 37 bp DNA PAT 26-JAN-2000  
DEFINITION Sequence 6 from Patent WO909211.  
ACCESSION A98888  
VERSION A98888.1 GI:6781847  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 37)  
AUTHORS Coutts,J.C. and Oultram,J.D.  
TITLE AMPLIFICATION OF NUCLEIC ACIDS  
JOURNAL Patent: WO 909211-A 6 25-FEB-1999;  
COUTTS JACQUELINE CLARE (GB); OULTRAM JOHN DOUGLAS (GB)  
FEATURES  
source 1..37  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 6 a 10 c 10 g 11 t

## ORIGIN

Query Match 57.3%; Score 12.6; DB 6; Length 37;  
Best Local Similarity 78.9%; Pred. No. 4.5e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ccgcctctcgacacatg 22  
||| ||||| |||  
Db 10 CCACTCTCTGACGTGA 28

## RESULT 6

LOCUS HCU84486 48 bp DNA INV 22-SEP-1997  
DEFINITION Haemonchus contortus CT microsatellite DNA sequence.  
ACCESSION U84486  
VERSION U84486.1 GI:2429139  
KEYWORDS  
SOURCE Haemonchus contortus.  
ORGANISM Haemonchus contortus.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Strongylida;  
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.

REFERENCE 1 (bases 20 to 29)  
AUTHORS Hoekstra, R., Criado-Fornelio, A., Fakeldi, J., Bergman, J. and Roos, M. H.

TITLE Microsatellites of the parasitic nematode Haemonchus contortus:  
polymorphism and linkage with a direct repeat  
Mol. Biochem. Parasitol. 89 (1), 97-107 (1997)  
97442739

JOURNAL 2 (bases 1 to 48)  
AUTHORS Hoekstra, R.  
TITLE Direct Submission  
SUBMITTED (09-JAN-1997) Institute for Animal Science and Health  
(ID-DIO), Molecular Recognition, Edelhertweg 15, Lelystad 8200 Ab,  
The Netherlands

FEATURES  
source 1. 48  
Location/Qualifiers

repeat\_region  
/organism="Haemonchus contortus"  
/db\_xref="taxon:6289"  
20. .29  
/note="microsatellite; imperfect"  
/rpt\_type=tandem  
/rpt\_unit=CT  
/evidence=experimental

BASE COUNT 14 a 15 c 6 g 13 t  
ORIGIN

Query Match 57.3%; Score 12.6; DB 3; Length 48;  
Best Local Similarity 78.9%; Pred. No. 4.5e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 2 accgcctctcgacacatg 20  
||| ||||| |||  
Db 19 ACTCTCTCTCAATATG 37

## RESULT 7

LOCUS I18948 58 bp DNA PAT 07-OCT-1996  
DEFINITION Sequence 30 from patent US 5501962.  
ACCESSION I18948  
VERSION I18948.1 GI:1599303  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 58)  
AUTHORS Bratford-Goldberg, S.R., Easton, A.M., Klein, B.K., McKearn, J.P. and Ollins, P.O.  
TITLE Interleukin-3 (IL-3) human/murine hybrid polypeptides and recombinant production of the same

JOURNAL Patent: US 5501962-A 30 26-MAR-1996;  
FEATURES Location/Qualifiers  
source 1. 58  
/organism="unknown"

BASE COUNT 13 a 20 c 15 g 10 t  
ORIGIN

Query Match 57.3%; Score 12.6; DB 6; Length 58;  
Best Local Similarity 78.9%; Pred. No. 4.5e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 caccgcctctcgacacat 19  
||| ||||| |||  
Db 14 CATCCGCTCTGCCCAAT 32

## RESULT 8

LOCUS I18949/c 58 bp DNA PAT 07-OCT-1996  
DEFINITION Sequence 31 from patent US 5501962.  
ACCESSION I18949  
VERSION I18949.1 GI:1599304  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 58)  
AUTHORS Bratford-Goldberg, S.R., Easton, A.M., Klein, B.K., McKearn, J.P. and Ollins, P.O.

TITLE Interleukin-3 (IL-3) human/murine hybrid polypeptides and recombinant production of the same  
Patent: US 5501962-A 31 26-MAR-1996;  
JOURNAL 1. 58  
FEATURES Location/Qualifiers  
source /organism="unknown"

BASE COUNT 11 a 14 c 19 g 14 t  
ORIGIN

Query Match 57.3%; Score 12.6; DB 6; Length 58;  
Best Local Similarity 78.9%; Pred. No. 4.5e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 caccgcctctcgacacat 19  
||| ||||| |||  
Db 49 CATCCGCTCTGCCCAAT 31

RESULT 9  
LOCUS I24133 58 bp DNA PAT 07-OCT-1996  
DEFINITION Sequence 30 from patent US 5543141.  
ACCESSION I24133  
VERSION I24133.1 GI:1604003  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 58)  
AUTHORS Bratford-Goldberg, S.R., Easton, A.M., Klein, B.K., McKearn, J.P. and Ollins, P.O.

TITLE Therapeutic methods using Interleukin-3 (IL-3) human/murine hybrid polypeptides  
Patent: US 5543141-A 30 06-AUG-1996;  
JOURNAL Location/Qualifiers  
FEATURES 1. 58  
source /organism="unknown"

BASE COUNT 13 a 20 c 15 g 10 t  
ORIGIN

Query Match 57.3%; Score 12.6; DB 6; Length 58;





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